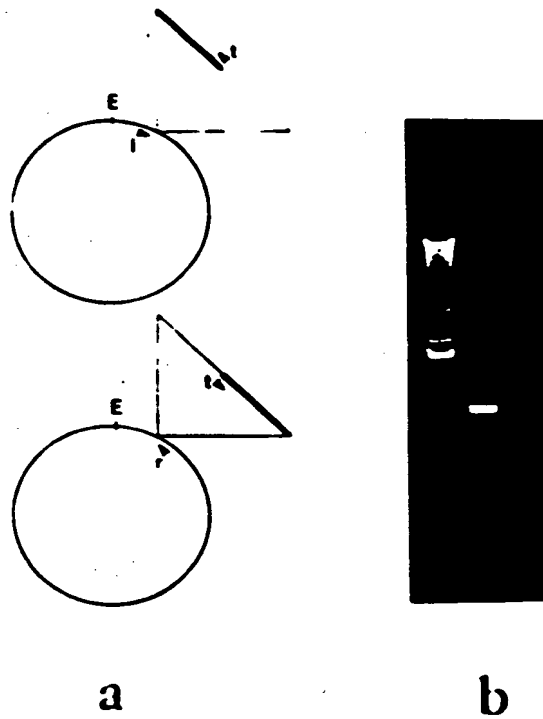


FIGURE 1

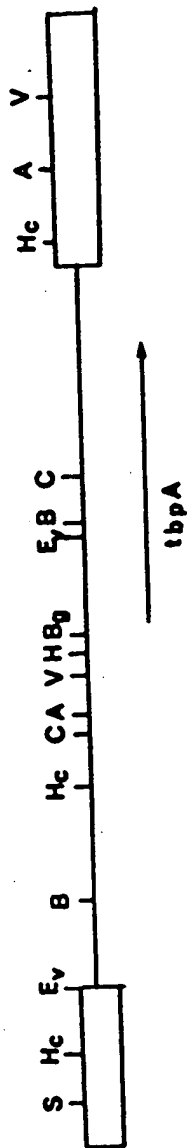


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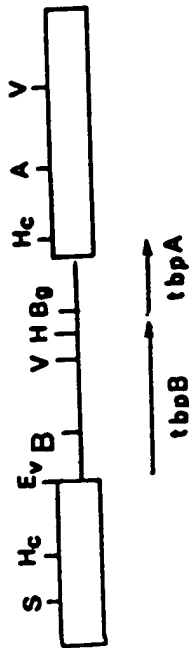
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FIGURE 2

Plasmid 9



Plasmid 10



Plasmid 482

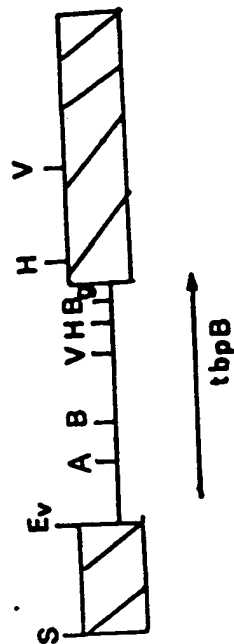


FIGURE 3

tbpB

10 20 30 40 50

1 CGCTTGCAGA TTTGTAAAAA ATTTAGCTAA AATCAGACCT GGCTTGTATT

51 TTAGGGTTAT TATGGAACAG ACAACGGAAC AAATAGATTA TAAATTATTA

101 AAGCATCGTT TTCGTGGCTA TTTACCGCTT GTGATTGATG TGGAACAGAG

151 GCTTAAATGC CCAAAGTGTG CCTTATTGGA ATTGGCCGGA ATTACTTTAA

201 AATTGGACGA GCCAAGGTTA TCTTATTGCC GGATTCAACA ATGCCAATTT

251 CCAATTTGCG GCCATTGGAG GGGGCGATTT TCAAGGGCCG AATATTTACC

301 CTCAGTCATT AAAATTCAAC GGCATTCATA TTCACAACC TCTAGAGGAA

351 GCGGTTTAGA GAATATTGCC CAATTCCCGG AAATGTTCAA AATGGTTTCG

401 AAAGCAATGA AGGAAGCAAG GCTGCCAACG GGCGGTGATT GTTGCCCCAC

451 AATGCCAGCG TTCGATCAGG GCTTTTTTAC AGGGCTGCGA TTAAACGGAA

501 TGCCAAGCGA GAGATCCCTT TCACCCTTTT GGCGATGTTT GACTACCGCC

551 GCCACCCTTT GCAGGTTTTA TGTTATGGGC AAACCGTGTT CGTTAAAAGC

601 CTGCCAGTGC AAAATCCGTT CACGTAGCAG CACTATAGGG CGAATTGGGT

651 ACCGGGCCCC CCTCGAGGTC GACGGTATCG ATAAAGCTTC ATATCGAATT

701 CCTGCAGCCC GGGGGATCCG ATGCGCCTTG CGGCTCAAGT TATTAGTGGC

751 ATCGGTTTTT TGGGTGATGG TGTCATTTTG CATAAGAAAA ATGATGCGAT

801 TTCAGGTTTA CCCACTGCGG CGATTATTTG GGCTTCTGCG GGGATCGGTA

851 TTGCTGCAGG GGAGGGTTTC GTGTTTCATG CGGTCATCGC CACTGTCATT

901 ATTTTGGTGT CTATTCGATT ATGTCCGTTG GTTCAACGTT GGGTTCATCG

951 TAAATCACAA CGTCGTCGAC GAAATATTCT TGTCAATGAT GCGGAAAGCA

1001 TACGGAAAGT TACCCAATTG TTATTCAATA ATCAGTATCG TATTGAACAT

1051 ATACAAGTCA AAGATCAAAG TAGTGGAGAA GTTGCCGGTT ACAAATTCGT

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FIGURE 3 CONT'D

1101 ATTGATTCCA CAATGTTCAA AGATGCGTAT GCTTTACTTA AAGCAGAAGA
1151 TGGCGAATAC TGTTCAAGTA GATATCATGA AAAAGAGTGC TTATATTCAA
1201 TTTTTTATTT TTTATTTAAT TTCTTTCCAC AAAAGATCAT TTTCAATTAT
1251 ATATACTGGA ATTTTGCCTT ACGCTATCTG TCATTTATTA TGCTATTCAA
1301 GCACAACAAA CTATGGAACA ACAATCAAAA TGTACGCTTA TCGGCTGCCG
1351 ATGATTTCTGA TAATGATCGA TGTGCAGAAA TATTTGAACT TACGATTTTC
1401 ACTGAGCAGT CAAAGCACGT TCGCGAGTAT CGACTCTACT TTATTTATCG
1451 TTTGTGCACT ATGTATAATC CACCTAATTC CGTGCCTTGG CCATAAAAGC
1501 CCCCTTCAAA TTGTATTTAT ATCAGCTACC GTGCCACCAT TCGTACTTTT
1551 CGGATCAAGA TTAAACAGA ATCCCTGCAT GCACAGCGAA ATCAGCTGCG
1601 GTATGCGAAA CGCCGCAGGA GCGCAGTACG CGAAGTGTAC CGTCACTATC
1651 AGTGCTAGAT TTGTCAATAA AAAATTAGTG ACCAAGCTTG GGTGCATAAT
1701 GATGGTGATG AAAGAACGCT CAATGCTTGA CACGTTGCAG GCTATCTGTA
1751 AGGGTATGGT AGTTACAGGC ACAGCCCAA CGGCCAATTG CTGGTTTTTT
1801 ATCCTTGATC CGAACAGTAC GAATGGTGGT CACGGTAGTG CATATACATA
1851 CTCAATTGAA GGGGGCTTTT ATGGCCCTAA GGCGACGGAA TTAGGTGGTA
1901 TTGTACATAG TGCAGAAACG GATAAAGATA GAGTCAGTAT TACATTCGGC
1951 GGAAAACGTC AAATAGAAAA ATAATCATAA TTCCCCTTTG CTGGTTGTAG
2001 ATAGCAGCGG GCAATTTTTT ATAAAAATTT GCAAAATTTA AATAA

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FIGURE 3 CONT'D

tbpa

10 20 30 40 50
1 AGACCCTATC TAATGATAAT GAAATATCAT CATTTTCGCT ATTCACCTGT
51 TGCCTTAACA GTGTTATTG CTCTTTCTCA TTCATACGGT GCTGCGACTG
101 AAAATAAAAA AATCGAAGAA AATAACGATC TAGCTGTTCT GGATGAAGTT
151 ATTGTGACAG AGAGCCATTA TGCTCACGAA CGTCAAAACG AAGTAACTGG
201 CTTGGGGAAA GTAGTGAAAA ATTATCACGA AATGAGTAAA AATCAAATTC
251 TTGGTATTCTG TGATTTAACT CGCTATGACC CTGGTATTTC GGTGGTGGA
301 CAAGGTCGCG GTGCAAGTAG TGGCTATGCC ATTCGAGGTG TAGATAAAAA
351 CCGTGTGAGC TTAATTGTTG ATGGGCTACC ACCAGCGCAC AGTTATCATA
401 CGCTGGTTCA GATGCTAATG GTGGTGCAAT TAATGAGATT GAGTATGAAA
451 ACATTCGTTT AATTGAGTTA AGCAAAGGAG CAAGTTCTGC GGAATATGGC
501 TCTGGTGCGC ATGGTGGTGC TATTGGTTTT CGTACTAAAG ATCGCCAGGA
551 TATTATTAAA GAGGGGCAGC ATTGGGGCTT ACATAGTAAG ACCTCTTATG
601 CCAGCAAAAA TAGCCATTTT TACAGTCTAT CGCAGCGGCT GGTGAGGCGG
651 GTGGTTTTCA AGCACTTGTT ATTGCAACTC ACCGACACGG TAAAGAGACC
701 AAAATTCATT CCGAGGCAAA TCAATTACAT ATTATTCGGC GTATAACCGG
751 CTTTCAAAAT CGCTACGACT TTACCCAATT CCGCACAGAA TGCCTCCTGG
801 AGGATCTTTT TTTATTGTGG AAGATACTTG CCCAACATTA GATTGTACTC
851 CTCGTGCAAG GGTTAAGTTG AACGCGATAA TTTCCAGTC AGAACATTTT
901 CGAATATACG CCTGGAAGAG GCGAAACAGC TTGAGATTCC TTATCGCACT
951 GAGCTCTCAG CCCAAAGAAT ARACCGGTAA AGATCGCATT GCACCAAACC
1001 CTTTAGATTA CAAGAGTAAT TCTGTTTTTA TGAAGTTTGG CTATCACTTT
1051 ACCTCGTCTC ATTATCTTGG CGCATCTCAC AAGATGATAC AAAACAACGG
1101 ACGATATCCG TCATSTGCAA ACGCCAGCTT ACTATACAAA AGACGATATT
1151 TACTTATCAC TTTGGAAC TA TTTTATCAA GGGGATATTA TTTAGATGGC
1201 TTAGTGTTCA AGCCAAGGAT CCCTTATGGG TTGCGCATAT GCCATGTGAA

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FIGURE 3 CONT'D

1251 CGTCACCACA AACGTCGTTT AGGATTCACC TATAAATATA AACCAGAGAA
1301 TAATCGCTGG TTGGATAGCA TTAACTCGTG CGTACGTGCT TTGCGCTCTC
1351 GCTGCTGTGC TCTGAGTAAA CAAGATATTG AACTATATAG CCGGCTACAT
1401 CGCTTGCAAT GTAGCGATTA TCCTGTGGTA GATAAAAATT GCGGCCCGAC
1451 TTTGGATAAA TCTGGTCTAT GTATCGAACT GAGCGTAATA ATTACCAAGA
1501 AAAGCATCGT GTCATTCATT TAGAATTGTA TAAAGCGCTA AATGCTGGTC
1551 AAGGCGTATT TAAGCAAACC CACAACTGA ATTTAGGCTT GGGCTTTGAA
1601 TCGATTAATC GCTTATGATC ATGGGGATAT GACTGCCCAA TATACCAAAG
1651 GCCGGTTATA CCAGCTACCG CGGAGAGGGG CTTTAGATAA TCCATATATT
1701 TATCGCCGCG ATCCACGCAG TATTGAAACG GTATCTTTGT GTAATAATAC
1751 AGCGGCGACA CTTAACTGTG ACGCGTTAAA TAAAGGCATA CGTTTGTACC
1801 TCCGCTGCAC TTAGGAACTA TAGTTTATGA AGGGGATAAT ATTTAGATGG
1851 CTTAGTGTTT AAGCAAGCAA GGATCCCTTA TGGGTTGCGC GATATGCCAT
1901 GTGAAGTTTT TGATGAACGT CACCACAAAC GTCGTTTAGG ATTCACACCT
1951 ATAAATATAT AAACCAGAGA ATAATCGCTG GTTGGATAGC ATTAACTCGT
2001 GCGTACGTGC TTTGCGCTCT CGCTGCTGTG CTGTGAGTTA AACAAGATAT
2051 TGAAACTTAT AGCCGGCTAC ATCGCTTGCA TTGTGAGCGA TTATCCTGTG
2101 GTAGTAGTAA AAATTGCGGC CCGACTTTGG ATAAATCTTG GTCTATGTAT
2151 CGAACTGAGC GTAATAATTA CCAAGAAAAG CATCGTGTCA TTCATTTAGA
2201 ATTTGATAAA GCGCTAAATG CTGGTCAAGG CGTATTTAAG CAAACCCACA
2251 AACTGAATTT AGGATTGGGC TTTGAATCGA TTAATTCGCT TATGGATCAT
2301 GGGGATATGA CTGCCCAATA TACCAAAGGC CGGTTATACC AGCTAACCGC
2351 GAGAGGGCGT TTAGATAATC CATATTTATC GCCGCGATCC ACGCAGTATT
2401 GAAACGGTAT CTTTGTGTAA TAATACACGC GCGACACTAA CTGTGACGCG
2451 TTAAATAAAG GCATACGTTT GTACCTCCGC TGCTGCCTAA TAAATCAAAA
2501 GAATAACCGA GATACGGTTC AGTGTTGTTC CAACCAGTTG CGATGGCCCA

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FIGURE 3 CONT'D

2551 CTACGTGAAC CATCACCCTA ATCAAGTTTT TTGGGGTCGA GGTGCCGTAA
2601 AGCACTTAAC CCTTCTGTCG TCTCCCGTGG ATGCTTAAAT TCGCAGCTAG

2651 TGGCAGGCAG GCACGTCACT CCTCTCGGTG ATTTCAGGTG CAACTGACCG
2701 GTTCTTGGTA CCACCCTTGA TATTAACCGG AGTCAATTAT AAAAACGAGT
2751 TACGTGGAGC GCAATTTATA ATGTCGATGT CAGATACTGT AAAACTCTAT
2801 ATTACCGTGG GCAGCAATTA GGTGACAGGG CCACGGGGCA AGCGAAACCA
2851 GACGGGTACC AATTACACCG ATTTGCCGCC CCCGGGAGAG AAATTTTCAGT
2901 TACCATTCAA AGAAGTTTAG AGCCGGCCAA AAGAAAATAC AAAAAACGCT
2951 GAAAGTATAT TCAGCGCGTT TTTGTTGCTC TAACGGATTA CATACGAATT
3001 CAAAATGTTT TAACGGTCGG TTA

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FIGURE 4

PHTBPB

CGCTTGCAGATTGTAAATAAATTAGCTAAATCAGACCTGGCTGTGTAATTTAGGGTTATTATG

-35

-10
Met

NGTBPB

TTTAAATAATAATAATAATATCCTTATCATTCCTTAATTGAATCGGGTTTGTATG

-35

-10
Met

NMTBPB

GTATTGCAGATTGTAAATAATAATAATATCCTTATCATTCCTTAAI TGAATTCGGTTTATATG

-35

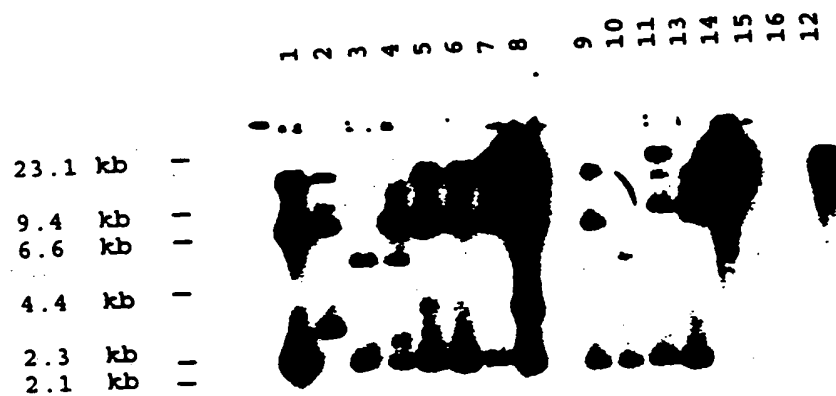
-10
Met

FIGURE 5



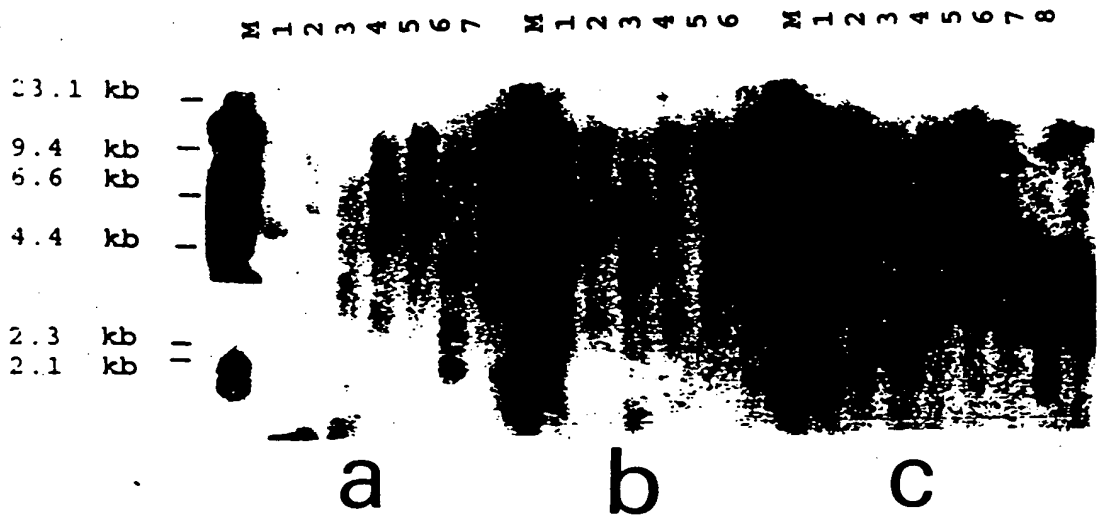
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FIGURE 6



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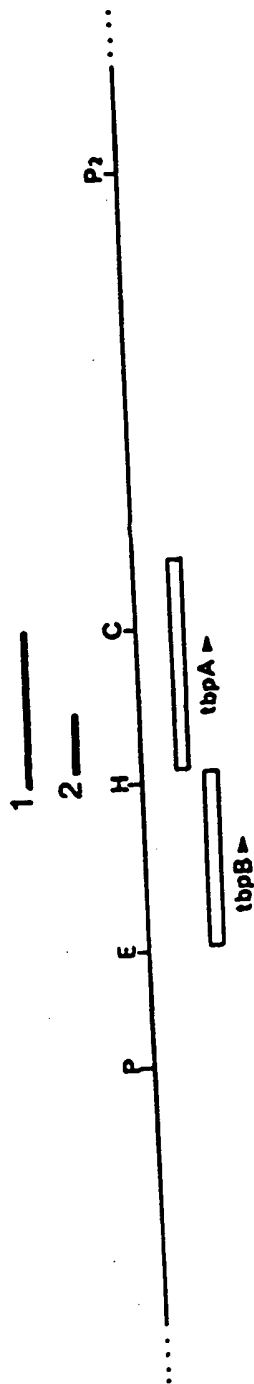
FIGURE 7



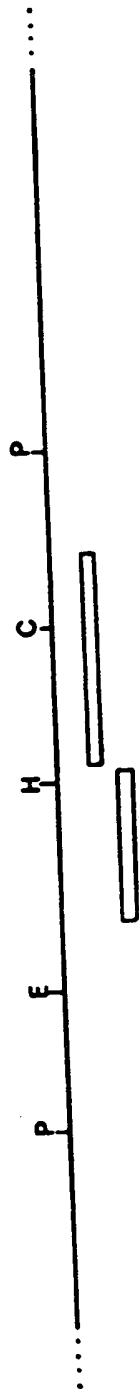
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FIGURE 8

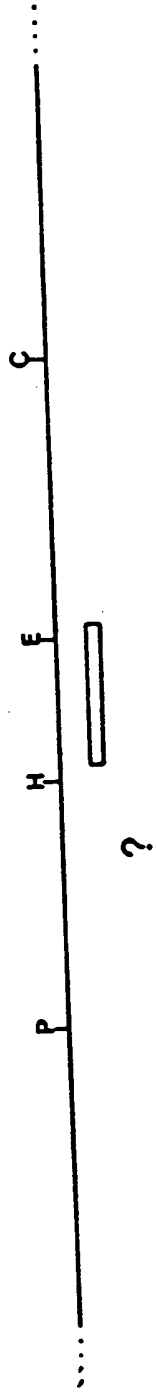
P. haemolytica A1



A. suis 3714



A. pleuropneumoniae CM5, Shope 4074



2 kb

FIGURE 9

PHTBP	MIMKYHHFRYSTVALTVLFALSHSYGAATENKKIENNDLAVLDEVIVTE	50
NGTBP1	MQQQ-HLFRNLCLSLMTALP-AYAENVQAGQAQEQKQ----LDTIQVKA	44
NM1	MQQQ-HLFRNLCLSLMTALP-VYAENVQABQAQEQKQ----LDTIQVKA	44
	* * * * *	
PHTBP	SHYAHERQNEVTGLGKVVKNYHEMSKNQILGIRDLTRYDPGISVVEQGRG	100
NGTBP1	KKQKTRRDNEVTGLGKLVKTADTLSEQVLDIRDLTRYDPGIAVVEQGRG	94
NM1	KKQKTRRDNEVTGLGKLVKSSDTLSKEQVLNIRDLTRYDPGIAVVEQGRG	94
	* * * * *	
PHTBP	ASSGYAIRGVDKNRVSLLDGLPQAHSYHT---LSGD---ANGGAINIEIE	144
NGTBP1	ASSGYSIRGMDKNRVSLTVDGLAQIQSYTAQAALGGTRTAGSSGAINIEIE	144
NM1	ASSGYSIRGMDKNRVSLTVDGVSQIQSYTAQAALGGTRTAGSSGAINIEIE	144
	* * * * *	
PHTBP	YENIRSIELSKGASSAEYSGAHGGAIGFRTKDAQDIIEKGQHWGLDSKT	194
NGTBP1	YENVKAVEISKGSNSVEQSGALAGSVAFQTKTADDVIGEGRWGIQSKT	194
NM1	YENVKAVEISKGSNSSEYNGALAGSVAFQTKTAADIIEGKQWGIQSKT	194
	* * * * *	
PHTBP	SYASKNSHFLQ-IAAAGEAGGFALVIATHRHGKETKIHSEANKLKHNR	243
NGTBP1	AYSGKNRGLTQSIALAGRIGGAELIIRTGRHAGEIRAHRAAGRGVQSPN	244
NM1	AYSGKDHALTQSLALAGRSAGAEALLIYTKRRGREIHAHKDAGKGVQSPN	244
	* * * * *	
PHTBP	RITGFENRYDFTQIPHMRPPGGS---FFIVEDTCPTLDCTPRARVKLNRD	290
NGTBP1	RLAPVDD-----GSKYAYFIVEEBECKNGGHE-KCKANPKKD	279
NM1	RLVLDEDKKE-----GGSQYRYFIVEEBECHNG-YA-ACKNKLKED	282
	* * * * *	
PHTBP	NFPVRTFPEYTPBERNAEQIPYRTEQLSAQEKTKGDRIAPNPLDYKSNSV	340
NGTBP1	VV-----GEDKRQT-----VSTRDYTGPNRFLADPLSYBSRSW	312
NM1	AS-----VKDERKT-----VSTQDYTGSNRLLANPLEYGSQSW	315
	* * * * *	
PHTBP	FMKFGYHFNSS-HYLGAILEDTKQR-TISVICKRQLTIQKTIPTYHLGTM	388
NGTBP1	LFRPGFRFENKRHYIGGILERTQQTFTDRDMTVPAPFLTKAVFDANQKQAG	362
NM1	LFRPGWHLDN-RHYVGAVLERTQQTFTDRDMTVPAYFTSEYVP-----G	359
	* * * * *	
PHTBP	FMKGIIFRWLSVQAK-DPLWVAHMPCEV-----DERHHKRLRGF	426
NGTBP1	SLRGNGNHKYAGNHKYGGLFTSGENNAFVGAEYGTGVFYDETHTKSRYGL	412
NM1	SLKGLG--KYSGDNKAERLFLVQEGGSTLQIGYGTGVFYDERHTKNRYGV	407
	* * * * *	
PHTBP	TYKY-KPENNRWLDINSVCVRALRSRCCALSKQDIELYSRLHRLHCSDP	475
NGTBP1	EYVYTNADKDTWAD---YARL-----SYDRQIGLDNHPQOOTHCSA-D	451
NM1	EYVYHNADKDTWAD---YARL-----SYDRQIGLDNRLQOOTHCSH-D	446
	* * * * *	
PHTBP	VVDKNCGPDLKSWSMYRTERNNYQEKHRVIHLEFDLALNAGQGVFLQTH	525
NGTBP1	GSDKYCRPSADKPFSSYKSDRVIYGESHKLLQAAPKKSFDATAK----IRH	497
NM1	GSDKNCRPDGKNPYSFYKSDRMIYBESRNLFAVFKKAFDATAK----IRH	492
	* * * * *	
PHTBP	KLNLGLGFESINSLMDHGDMTAQYTLGRLYQL---PRRDRPSIWTVSLCN	572
NGTBP1	NLSVNLGYDRFGSNLRHQDYQYQSAN-RAYSLKTPPONNGKKTSPNGREK	546
NM1	NLSINLGYDRFKSQLSHSDYYLQNAV-QAYDLITPK----KPPFPNGSKD	537
	* * * * *	

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FIGURE 9 CONT'D

PHTBP	NT-----RATLNC DAL-NLGIRLYLRCCLINQLNNPRYGSVLFPQFGRV	615
NGTBP1	NPYWVSIGRGNVVTROICLFGNNTYTDCTPRSINGKSYAAV--RDNVRL	594
NM1	NPYRVSIGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYAAV--QDNVRL	585
	*	
PHTBP	HRTWTPTSLGELPSIRAMAHYVNHHPNQVFWGRGAVKHLT-----LLSS	659
NGTBP1	GR-WADVGAG----LRY--DYRSTHSDGSGVSTGTHRTL SWNAGIVLKPA	637
NM1	GR-WADVGAG----IRY--DYRSTHSEDKSVSTGTHRNLSWNAGVVLKPF	628
	*	
PHTBP	PWM-LKFAASG--RHVTLSVISG-ATDRFLVPPLILTGVNYKNES---YV	702
NGTBP1	DWLDLT YRTSTGFRLPSFAEMYGWRSGDKIKAVKIDPEKSFNKEAGIVFK	687
NM1	TWMDLT YRASTGFRLPSFAEMYGWRAGESLKTLDLKPEKSFNREAGIVFK	678
	*	
PHTBP	SAIYNVDVRYCKTLY-----YRGOOLGDRATGQAKPDGY---QLHRFA	742
NGTBP1	GDFGNLEASWFNNAYRDLIVRGYEAQIKDGKEQVKGNP-AYLNAQSARIT	736
NM1	GDFGNLEASYFNNAYRDLIAPGYETRTQNGQTSASGDP-GYRNAQNARIA	727
	*	
PHTBP	APG-----RNFSYHKKFRPAK---ENTKNAESIFS	770
NGTBP1	GINILGKIDWNGVWDKLEPGWYSTFAYNRVRVVDIKKRADRTDIQSHLFD	786
NM1	GINILGKIDWHGVWGGLPDGLYSTLAYNRIVKDADIRADRTFVTSYLPD	777
	*	
PHTBP	A-----FFVGSNGLHTNSKSCFNGLHEPIPYFFNFLRNVPFRFNEYHCCC	815
NGTBP1	AIQPSRYVVGSGYDQPEGKWGVNGMLT-----YSKAKEITELLGSR---	827
NM1	AVQPSRYVLGLGYDHPDGIWINTMFT-----YSKAKSVDELLGSQ---	818
	*	
PHTBP	TSLIAASILHHIYHWVDFRYYYYFV--YFCWILHHLIHINSFLMLLSHY	863
NGTBP1	-ALLNGNSRNTKATARRTRPWYIVDVSGYYTVKKHFTLRAGVYNLLNHRY	876
NM1	-ALLNGNANAKKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRY	867
	*	
PHTBP	--REVVYLTCACAFNIVTVNGF----CVGCCSNILAEMKF	898
NGTBP1	VTWENVRQTAAGAVNQHKQVGVYNRYAAPGRNYTFSLEMKF	917
NM1	VTWENVRQTAGGAVNQHKQVGVYNRYAAPGRNYTFSLEMKF	908
	*	

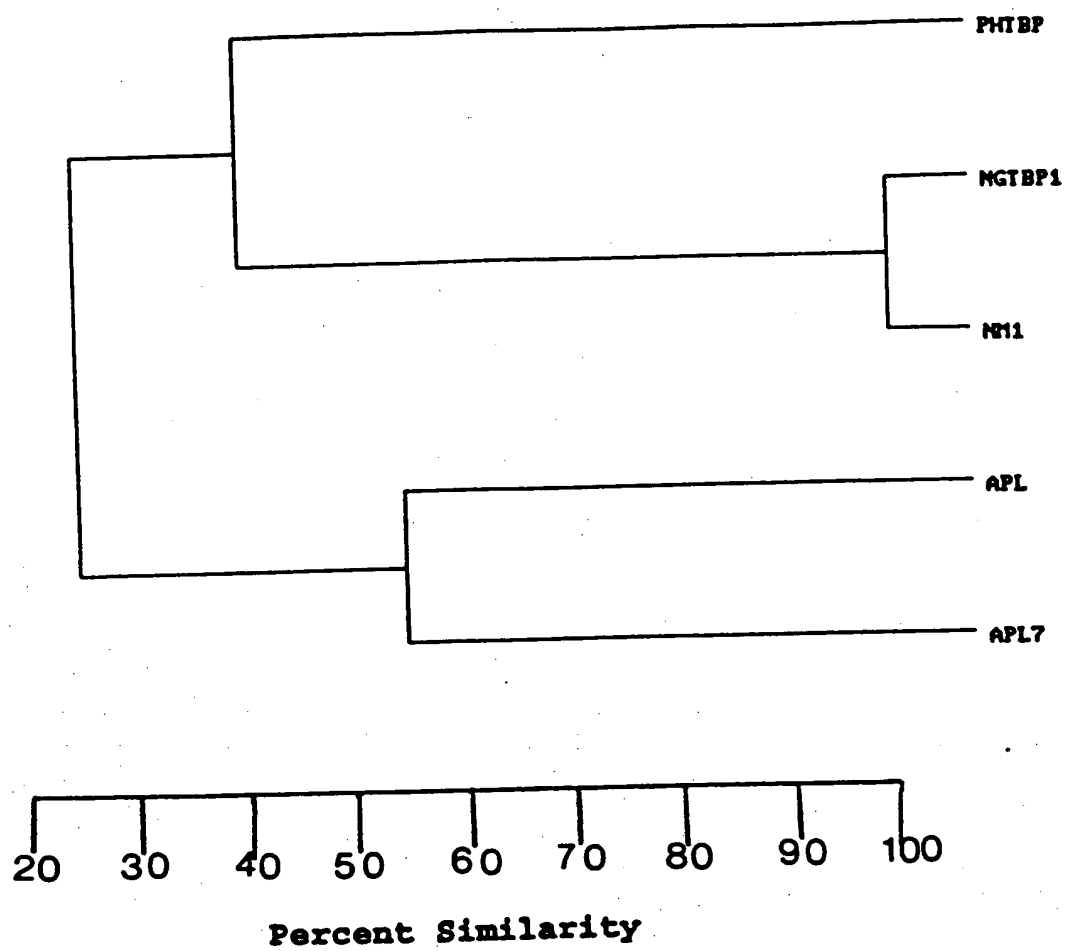
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FIGURE 10

PHTBP1	MIMKYHFRYSTVALTVLPALSHSYGAATENKKIERNNDLAVLDEVIVTE	50
APL	MHPKLNPY---ALAPTSPLVACSGGKGSFD-----LEDVRPNQ	36
APL7	MHPKLNPY---ALAPTSPLVACSGGKGSFD-----LEDVRPNK	36
	*	
PHTBP1	SHYAHERQNEVTGLKVVVNYHEMSK--NQILG--IRDTRYDPGISVVE	96
APL	TAKAEKATTSYQDEBTKKKTKEBELDKMEPALGYETQILRRNKAPKTETG	86
APL7	TTGVSKEE--YKDVETAKKEBQLGELMEPALGYVVKV-----FVSSFE	78
	*	
PHTBP1	QGRGASSGYAIRGVDKNRVSLLDVGLPOAHSYHTLSGDANGGAINET--EY	145
APL	EKRNER-----VVELSEDKITKLYQESVEIIPH--LDELNGKTTSDNVYHS	130
APL7	NKK-----VDISD-----IEVITNGNLDDVPYKANSSK--YNY	109
	*	
PHTBP1	ENIRSIELSKGASSAEYGGSGAHGGAIGFRTKDAQ-DIIEKG-----	185
APL	HDSKRLDKNRDLKYVRSGYVYDGSFNEIRRNDSGFHVFKQIDGYVYYLG	180
APL7	PDIK--TKDSSLQYVRSGYVIDGEHSGSNEK-----GYVYYKG	145
	*	
PHTBP1	----QHWGLDSKTSYASKNSHFLQIAAAGEAGGFALVLIATRH-----	225
APL	VTPSKELPKGKVISYKGTWDFVSNINLEREIDGFDTSGDGKNVSATSITE	230
APL7	NSPAKELPVNQLLTYTGSDWFTSNANLANE-----BGRPNYLANDDYTK	189
	*	
PHTBP1	--GKETKI--HSEANKLKHNRITGFPENRYDFTQIPHRMPPGGSFFIVED	272
APL	TVNRDHKVGEKLGDNVKGVAHSSEFAVDNKKLTGSLYRNG--YINRN	278
APL7	FIGK--RVGLVSGDAKPAKHYTSQFEVDFATKMTGK-----SD	228
	*	
PHTBP1	TCPTLDCTPRARVKLNDRNDFVVRTFPETPEERNABQIPYRTEQ--LSAQ	320
APL	KAEVTKRYSIEADIAGNRFRG-----KAKAEKAGDPIFT--DSNYLEGG	321
APL7	KEKTI---YTVNADIRGNRFTGAATASDNKKGKGSYNFFSADSQSLEGG	275
	*	
PHTBP1	EKTGKDRIAFNPLDYKSNSVFMKFGYHFNSSHYLGAILEDTKQRTISVIC	370
APL	FYGPKAEMAGKFFTNKSLFAVFAAKSENGETTTTERIIDATKIDLTQFN	371
APL7	FYGPKAEMAGKFFVANDKSLFAVFAKENGSNVNTVRIIDASKIDLTNFS	325
	*	
PHTBP1	KRQLTI--QKTIILTYHLGTMFMKGIIFRWLSVQAKDPLWVAIMPCEVDER	418
APL	AKELNNFGDASVLIIDGQKIDLAGVNFNKSKEVEINGKTMVAVACCSNLE	421
APL7	ISELNNFGDASVLIIDGKKIKLAGSGFTNKETIEINGKTMVAVACCSNLE	375
	*	
PHTBP1	HMKRRLGFTYKYKPPENNRWLDINSVCVRLRSRCCALSKODIELY-----	463
APL	YMK-----FGQLWQKEGKQVKNLSLFLQGERTATDKMPAGGNYKYVGTWD	467
APL7	YMK-----FGQLWQABGGKPPENNSLFLQGERTATDKMPKGGNYKYIGTWD	421
	*	
PHTBP1	---SRLHRLHCSDFPVVDKNCGPTLDKSNWYRTERNNYQEKATCHSPCI	510
APL	ALVSKGTNWIAADNNRESGYRTEFDVNFSDKKVNGKLFDKGGVNPVFTV	517
APL7	AQVSKENNWVATADDORKAGYRTEFDVDFGNKHLGKLFDKGVPNPVFTV	471
	*	
PHTBP1	LKALNAGQGVFKQTHKLNGLGFESNLIRLTIIGIILPNIPKAGYTSYRG	560
APL	DATIN--GNGFIGSAKTSDSGFALDAGSSQHGNAVPSDIKVNNGFYGP--T	564
APL7	DAKID--GNGFTGAKTSDGFFALDSGSSRYENVKPNVAVSOGFYGP--T	518
	*	
PHTBP1	RGRLDNPIYRRDPRSIETVSLCNRATLTLRLVNVKGIIRLLLR	604
APL	AGELGQGFHHKSDNGSVGAV-----FGAKRQIE---K	593
APL7	AGELGQGFHHKSENGSVGAV-----FGAKQOVK---K	547
	*	

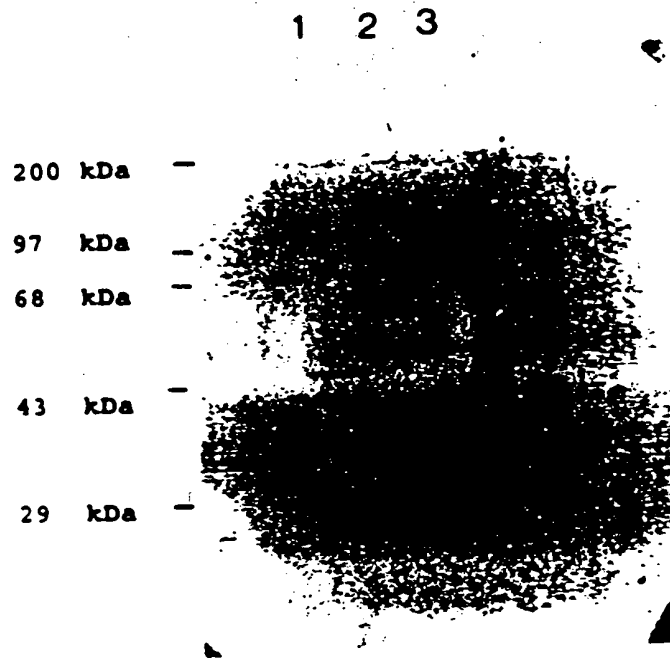
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FIGURE 11



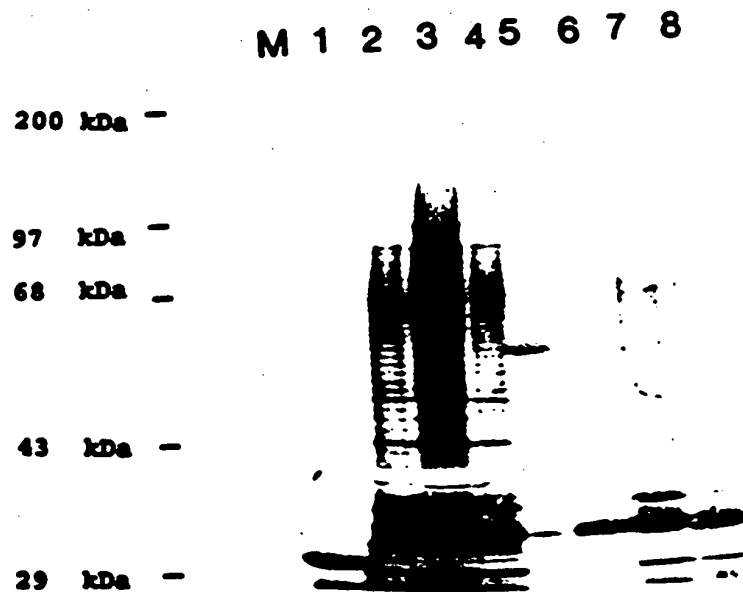
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FIGURE 13



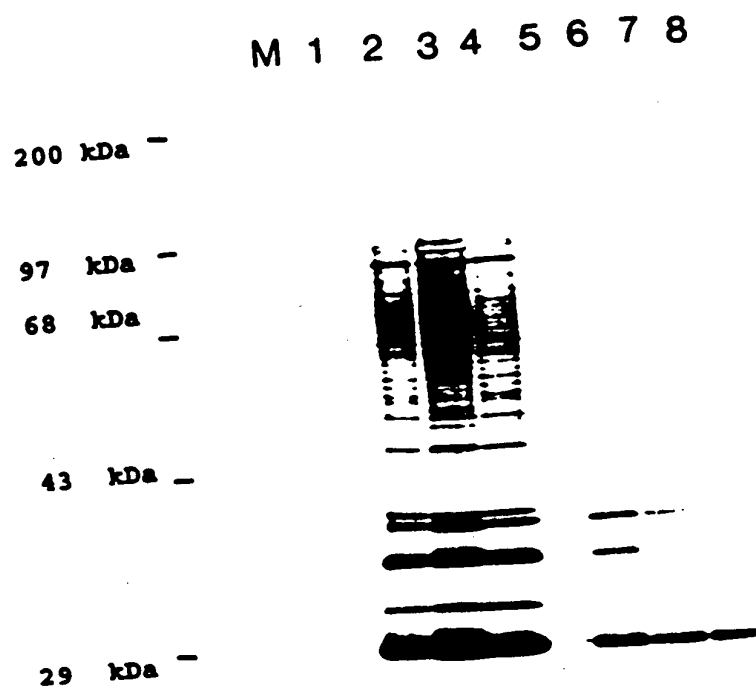
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FIGURE 14



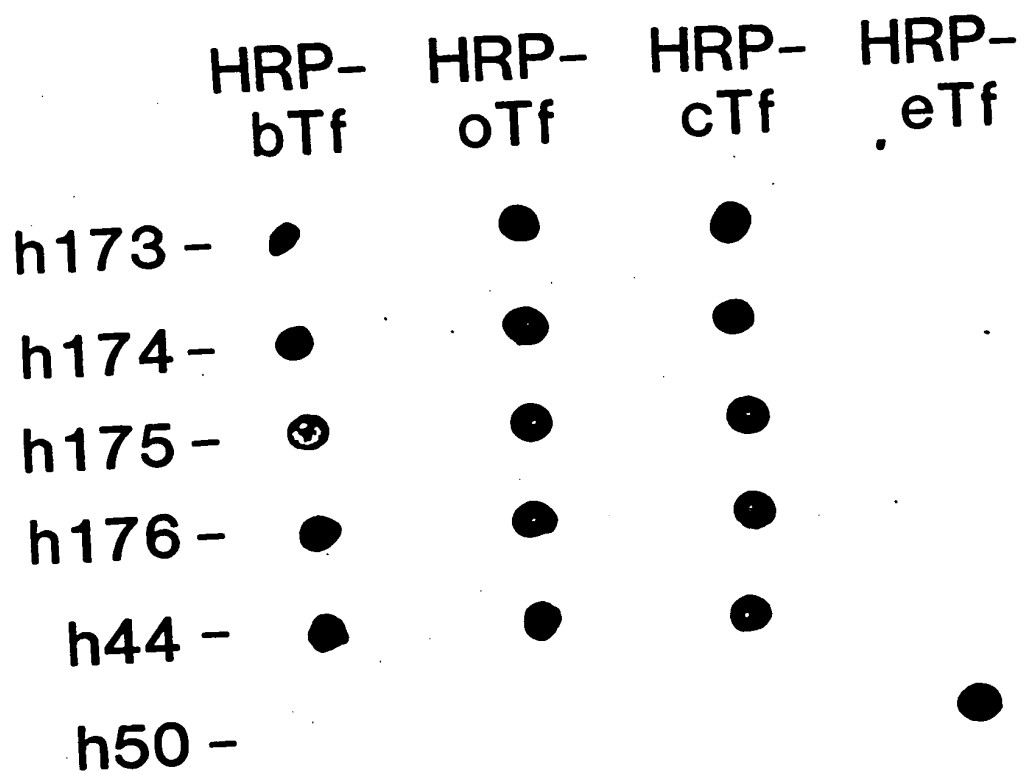
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FIGURE 15



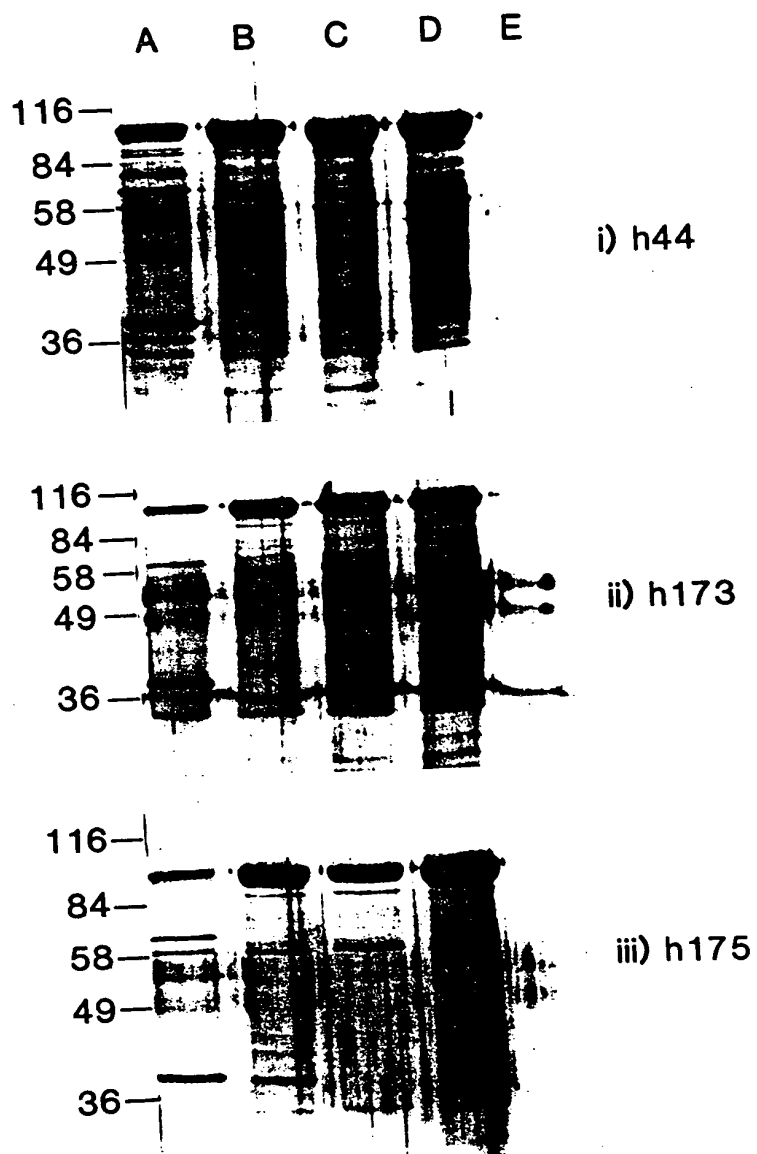
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FIGURE 16



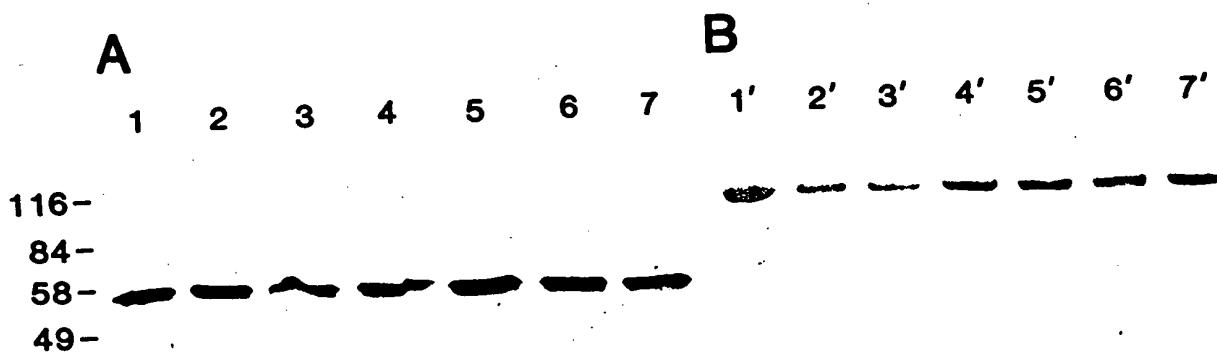
9662T" 05455280

FIGURE 17



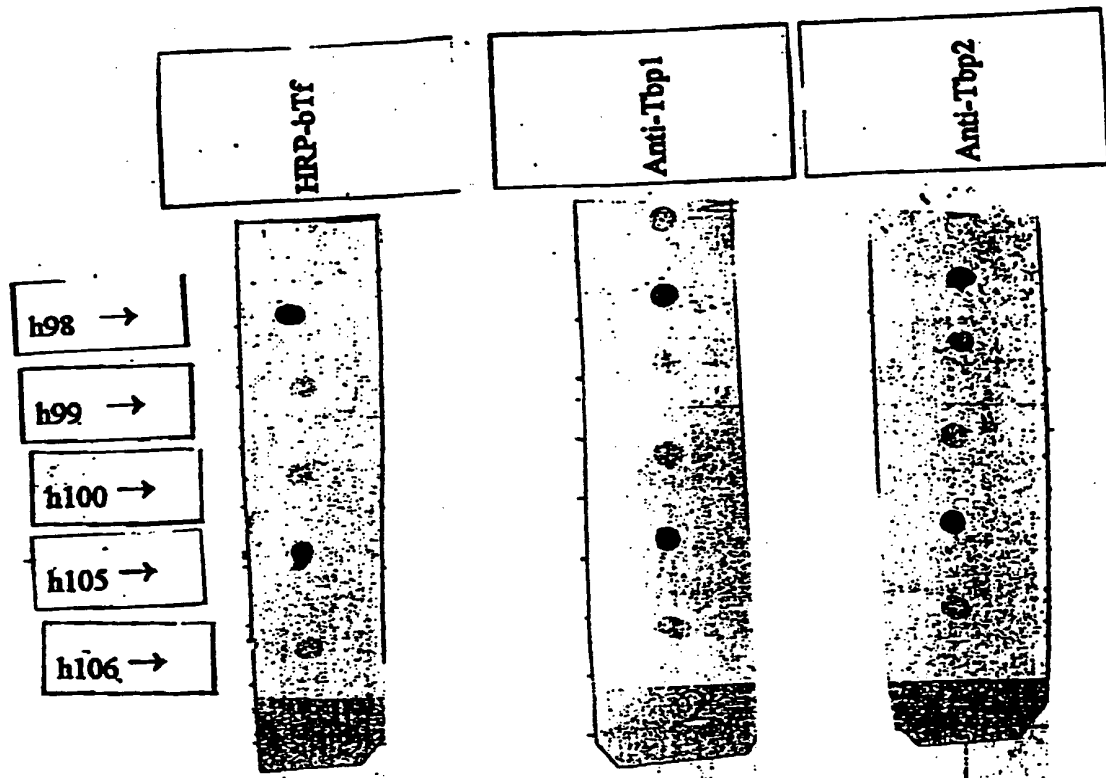
08753750.112996

FIGURE 18



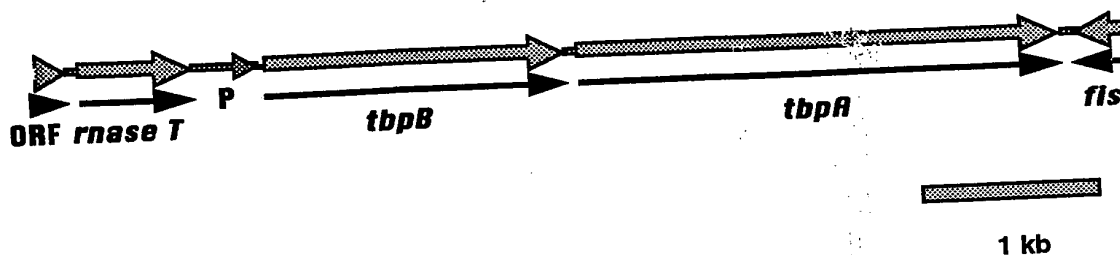
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FIGURE 19



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FIGURE 20



1168
 ATTTTTTATCTAATCTAAAAACAAGCGTTTCCACCTTGGAAATGATTAACATGATC
 CTGAAACTAATAAAGTTCAAACCTTTACATTAAAGTTTATATTATAAATTATAATGA
 -35 -10
 TTATTATTTTATAAATTAAAGGAGACATTATGTTTAAACTTAAAAGTAGTTTGTGTA
 SD Met₁₃₀₉
 CTG.....*tbpB*.....GAAAAATAATCATAATCCCCCTTTGCTGGTTGTAG
 SC₃₀₆₃
 ATAGCAAGCGGGCAATTTTTTATAAAAATTTGCAAAATTTAAATAAAGGAGACCCT
 SD
 ATCTAATGATAATGAAATATCATCATTTTCGC.....*tbpA*.....AGAAA
 Met₃₁₅₁
 TTTTCAGTTTAGCATTTGAAATGAAGTTTTAG.
 SC₅₉₄₃

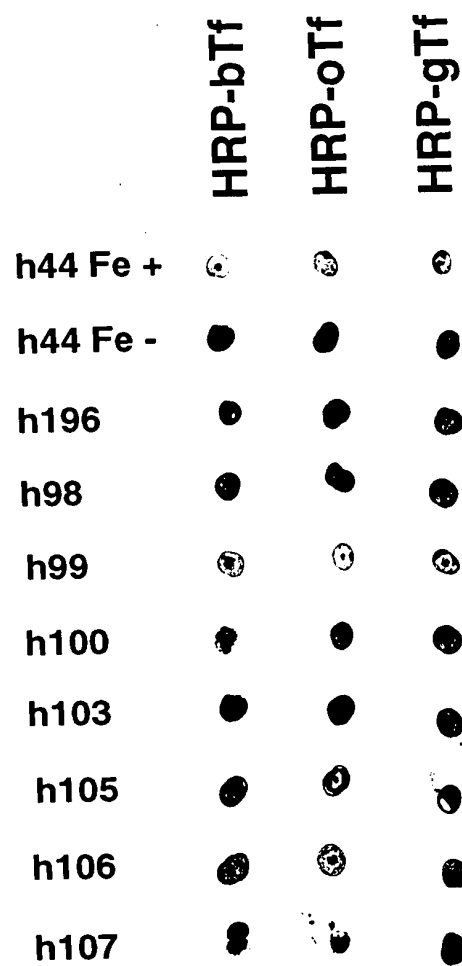
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FIGURE 23

ATGTTTAAACTTAAAAGTAGTTTTGTACTGCTTAATGCGGCGCTACTTGCTGCTTGTTCCCT
CAAATGGTGGAAGCTTTGATGTTCAATCTGCCAAAGTTGAATCTCAAACGCAAACCTACCCC
CAAAAAGCCAAGTTTACAAGATGATAATAGTAACGCAAGACGTACAGTAAGCGCTTCTGAA
ACTGAAGCTTTATTCAGCCGGGGTTTTGGTTTTTTCAGCCAAAATTCGCGCTCGTAATCTCC
TTCCGCAGGGGAAGGAAGATGTAGCCCCCTATTGGTGATATAAAAAGAGATTACTGGAGATCT
GCCAAAATTCGGTATGAAGAAGAGGTTAAAGCGTGCGGTAGTAGTGCTGATGGATTTAGC
CATACTCATGATAGAAATCATAAGTTGTATACAAGAGATTTTAATTTTGTTCGTTCCGGCT
ATGTTGTGCATTCTGGTCCAAAACCTGAAATAAAGCCATAAGAAATTTTGAGAACAGGTGC
ACATGGGTATGTTTACTATTTAGGTATAGAGCCGCCCAAAGCAATACCTACCCAAAACTA
ACTTATAAAGGATATTGGGATTTTACTACCTATGCGGCTAAGGGGAGAGATAGTAATATTT
TTCTAATTCGCGCAGGCATCAATAGTGGCGCCATACCGGAAAATAGTCACGATATTAATGT
TGATGATTCTGAAAAACCAATGGGGCATAAGGAGAAATTTACGGCTGATTTTGCTAATAAA
ACTTTAACTGGAACATTGGTTTCGTAATGGGTATGTTAGTCGTAGCAAAGAGCAAAAAATTA
CAACAATTTACGATATTGATGCGAAAATTAAGGTAATCGCTTTTCTGGTAAAGCAAACCC
AAAAAAACCGATGATCCTTATTTTGGGAAAAGCTCCACGACACTTGAAGGTGGATTTTTT
GGTGGGGAGGCTCAAGAACTTGCCGGTAAATTCCTAGCTGATGATAAGTCGGTATTTGTTG
TTTTTGGCTGGCACACGAGATGCTAAAAAAGATGATAGTGAATCTGCCTTTGATGCTTTCCC
AATTAAACTTAAAGATTTAAATAAATCTGAGATGGATACTTTTCGGGAATGCGACACATTTG
ATTATTAACAATAAGCAGATTCCACTTATTGCGGAAGCCACAAAAGCTTTGCCGAGATGA
AATTTGATGATTTGGTTACCCGTACTATTGATGGAAAACGTATCGAGTTTCAGTCTGCTG
TAATAATTTAGATTATGTCAAATTTGGGATTTATAGCGAGGGAAATAATAGTGATACTGCT
CTCCAAGAATATTTAGTAGGAGAACGTACAGCTCTGGCAGATTTGCCAACAGGGACAGTAA
AATATCGAGGTACTTGGGACGGGGTAATGTACAGTAAATCTGGCTCGGCAGGGGTTGAATC
GCCAAGTAACAGCGAAAGTGTAATCTGTTCACTATTTCGATGTAGATTTTGTCAATAAAAAA
ATTAATGGCAAGCTGATTGCTAATGATGGTGTTGAAGAACGCCCCAATGCTGACACTGGAAG
GCAATCTGAAAGGGAATGGTTTTGGAGGCACAGCCAAAACGGGCAATTCTGGTTTTAATCT
TGATCCCAAAAGTACGAATGGTGGCACGGTAGGGCATATAAATACTCAATTTGAAGGGGGC
TTTTATGGCCCTAAGGCGACGGAATTAGGTGGTATTGTACAAAATACAGAAACGGATAAAG
ATAGAGTCAGTATTACATTCGGCGGAAAACGTCAAATAGAAAAATAA

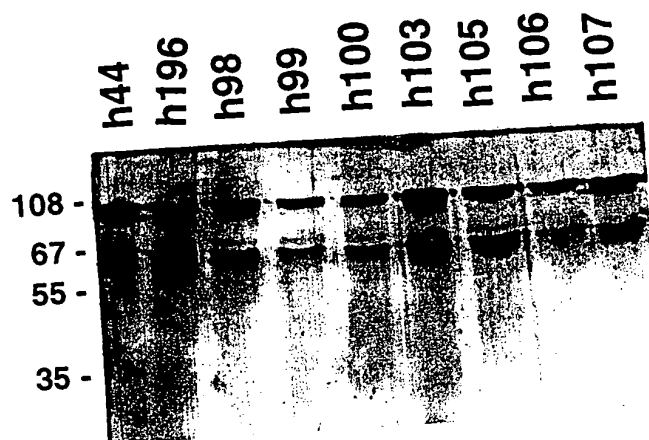
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FIGURE 25

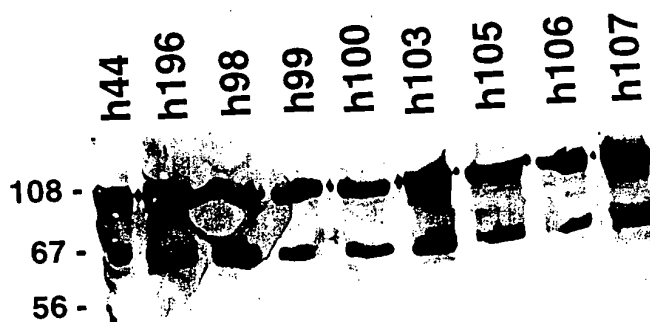


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FIGURE 26



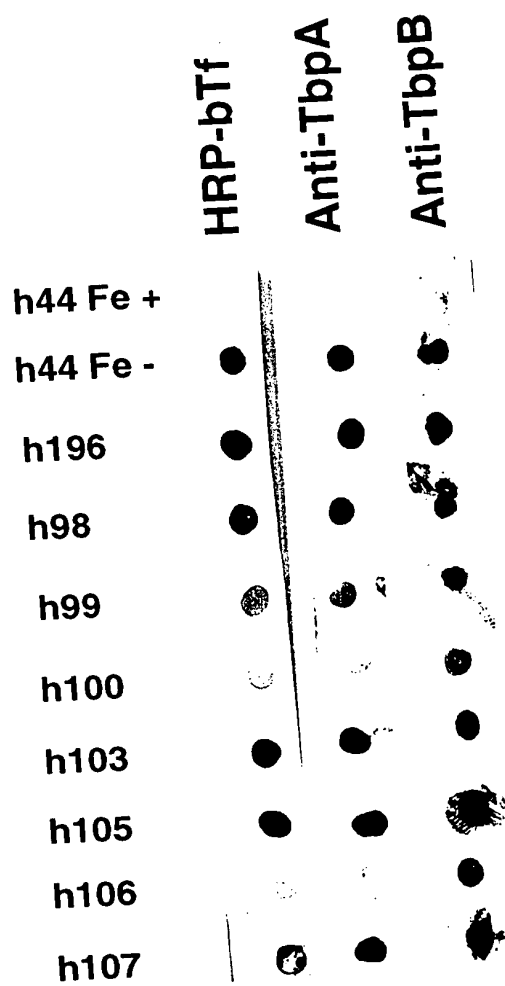
A



B

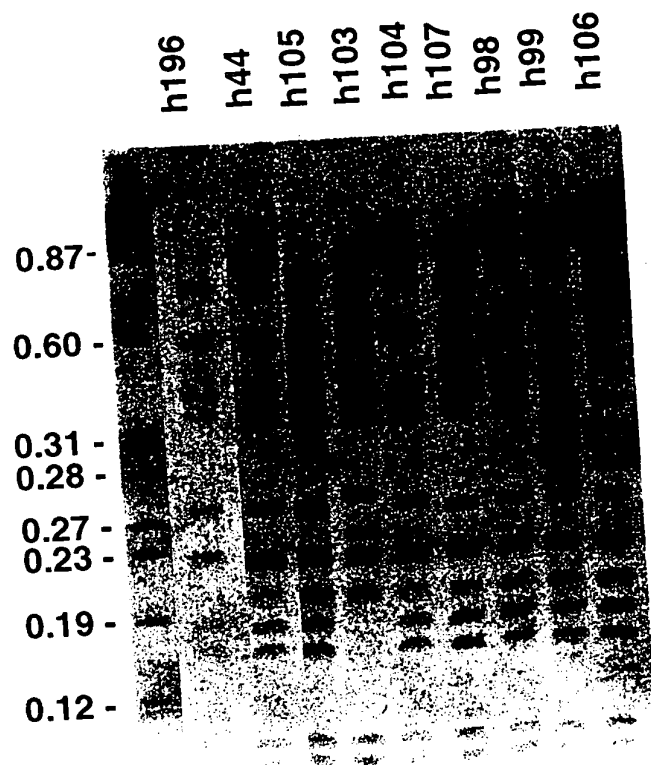
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FIGURE 27

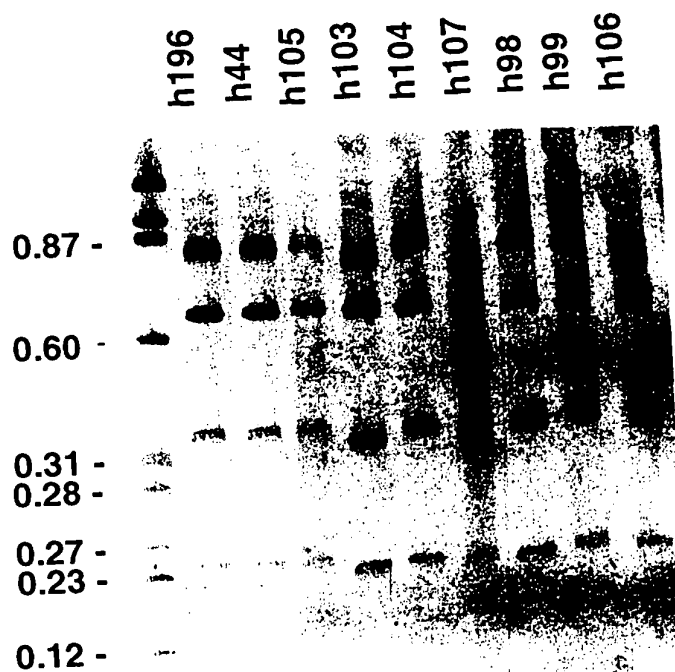


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FIGURE 28



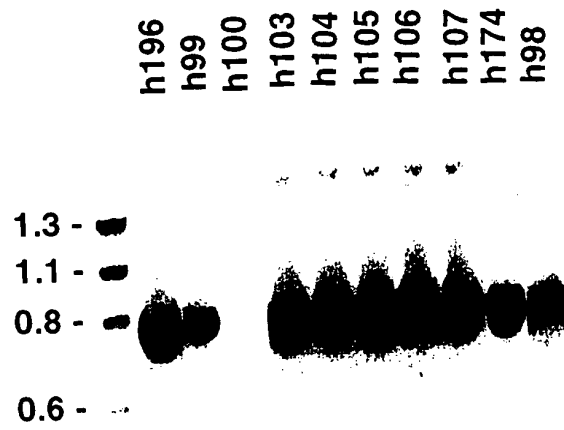
A



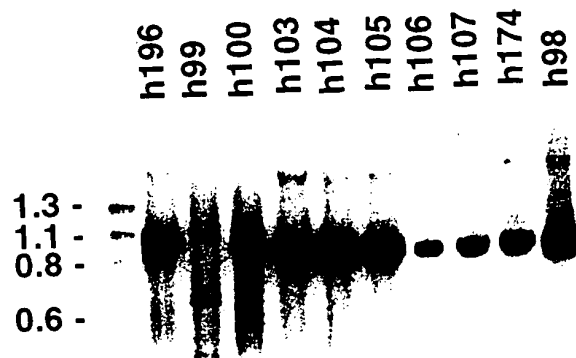
B

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FIGURE 29



A



B

9662T" 054E5480